

Appl. No. 10/027,000
Amdt. dated April 11, 2005
Reply to Office Action of October 19, 2004

IN THE SPECIFICATION:

Please amend the paragraph at page 18, lines 26-29 as follows:

A Basic BLASTN search (<http://www.ncbi.nlm.nih.gov/BLAST> on the worldwide web) of the non-redundant nucleic acid sequence database was conducted on September 11, 2001, with the *bgl4* gene sequence presented in Figure 1 (SEQ ID NO:1), indicated no sequences producing significant alignments (i.e. with an E value of less than 10^{-6}).

Please amend the paragraph at page 24, lines 1-12 as follows:

A Basic BLASTP search (<http://www.ncbi.nlm.nih.gov/BLAST> on the worldwide web) of the non-redundant protein database, conducted on September 11, 2001 with the BGL4 amino acid sequence indicated 46% sequence identity to GenBank Accession Number X05918 (beta-glucosidase precursor of *Kluyveromyces marxianus*), 45% sequence identity to GenBank Accession Number AL355920 (beta-glucosidase precursor of *Schizosaccharomyces pombe*), 42% sequence identity to GenBank Accession Number AF329731 (beta-glucosidase of *Volvariella volvacea*), and 41% sequence identity to GenBank Accession Number AJ293760 (putative beta-glucosidase of *Agaricus bisporus*). The ten sequences having highest identity but less than 46% identity with BGL4 were all annotated as beta-glucosidases. These sequence similarities indicate that BGL4 is a member of glycosyl hydrolase family 3 (Henrissat, B. and Bairoch, A. (1993) Biochem. J. 293:781-788).

Please amend the paragraph at page 28, lines 26-30 as follows:

Preferred culture conditions for a given filamentous fungus may be found in the scientific literature and/or from the source of the fungi such as the American Type Culture Collection (ATCC; "<http://www.atcc.org/>" on the worldwide web). After fungal growth has been established, the cells are exposed to conditions effective to cause or permit the over expression of BGL4.

Please amend the paragraph at page 37, lines 21-25 as follows:

Exemplary computer programs which can be used to determine identity between two

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sequences include, but are not limited to, the suite of BLAST programs, e.g., BLASTN, BLASTX, and TBLASTX, BLASTP and TBLASTN, publicly available on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/> on the worldwide web. See also, Altschul, *et al.*, 1990 and Altschul, *et al.*, 1997.